

Wing geometric morphometrics of European honey bee populations

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INTRODUCTION



Wing venation patterns can be used to identify honey bee subspecies. Geometric morphometrics, a more precise approach, requires the annotation of 19 landmarks on the forewing vein junctions. The software DeepWings© automates geometric morphometric analysis of forewings, enhancing accuracy and speed for large-scale studies. Our main objectives are to assess (i) how closely the colonies identified by DeepWings© match the endemic evolutionary lineages and subspecies, and (ii) the association between the identification produced by DeepWings© and that inferred from mitochondrial DNA.

METHODS

Sampling: 827 colonies, 29 European countries.



Five workers per colony



Rigth forewing



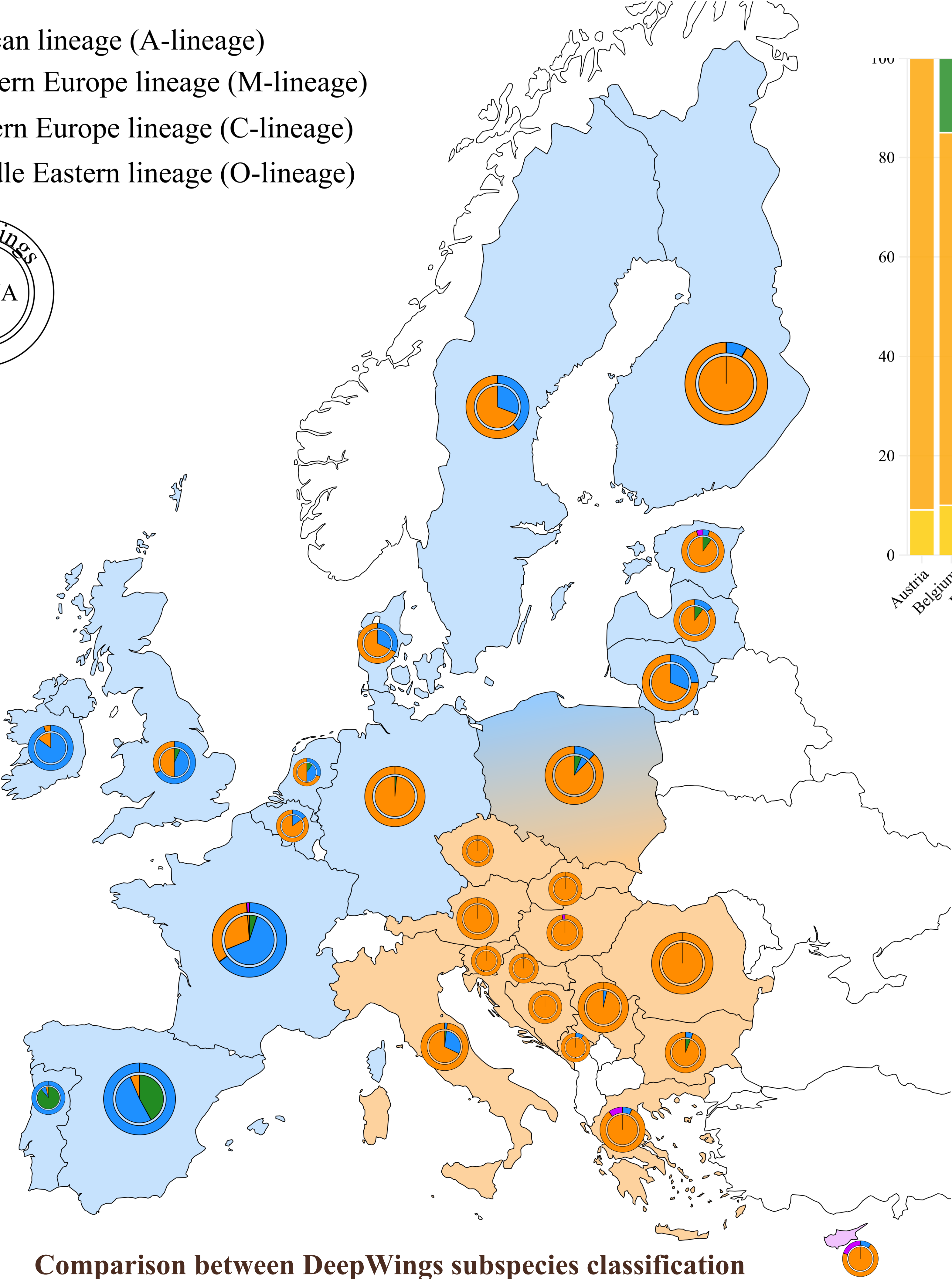
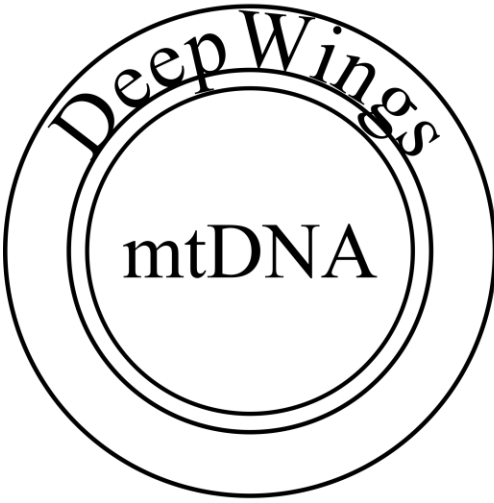
Stereomicroscope



DeepWings© classification

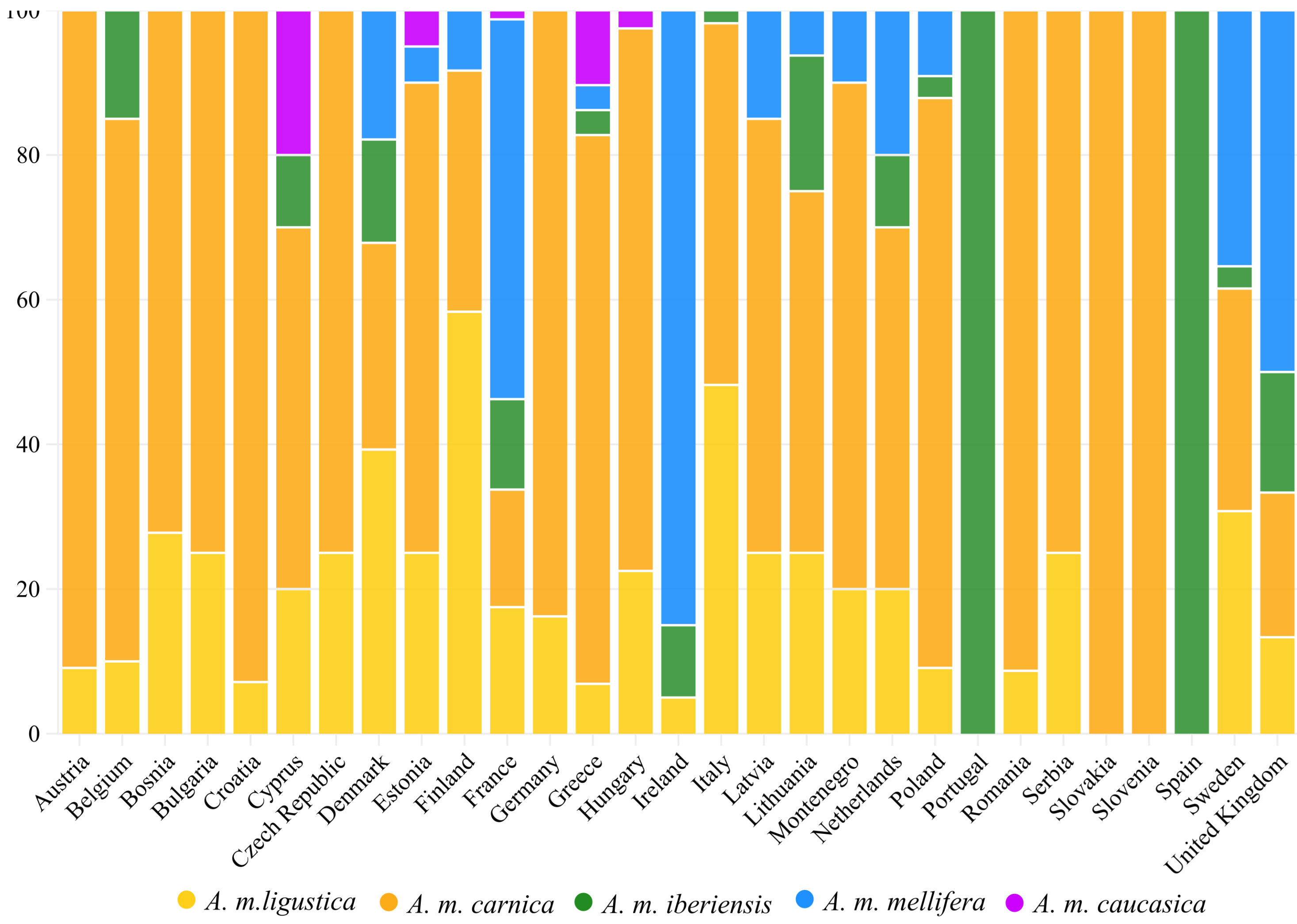


- African lineage (A-lineage)
- Western Europe lineage (M-lineage)
- Eastern Europe lineage (C-lineage)
- Middle Eastern lineage (O-lineage)



Comparison between DeepWings subspecies classification (outer ring) and mtDNA lineages (inner ring)

DeepWings subspecies classification



Native evolutionary lineages *sensu* Ruttner 1988:

C: Austria, Bosnia, Bulgaria, Croatia, Czech Republic, Greece, Hungary, Italy, Montenegro, Romania, Serbia, Slovakia, Slovenia, Poland.

M: Belgium, Denmark, Estonia, Finland, France, Germany, Ireland, Latvia, Lithuania, Netherlands, Portugal, Spain, Sweden, United Kingdom, Poland.

O: Cyprus.

This analysis of mtDNA and wing morphology across Europe yielded predominantly similar results, emphasizing the dominance of C-lineage genetic variation and highlighting the need for strategic conservation efforts to preserve the native genetic diversity of *Apis mellifera* in each country.

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